

ATTACHED TO
#10

SEQUENCE LISTING

<110> DORKEN, Bernd
RIETHMULLER, Gert
KUFER, Peter
LUTTERBUSE, Ralf
BARGOU, Ralf
LOFFLER, Anja

<120> CD19XCD3 SPECIFIC POLYPEPTIDES AND USES THEREOF

<130> 028622/0102

<140> US 09/673,735

<141> 2000-12-27

<150> PCT/EP99/02693

<151> 1999-04-21

<150> EP 98107269.7

<151> 1998-04-21

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

gaagcacgcg tagatatckt gmtcacccaa wctcca

36

<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 2

gaagatggat ccagcggccg cagcatcagc

30

<210> 3

<211> 33

<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 3
cagccggcca tggcgcaagg scagctgcag sag 33

<210> 4
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
accaggggcc agtggataga caagcttggg tgtcgaaaa 39

<210> 5
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
aggtgtacac tccatatcca gctgaccagg tctcca 36

<210> 6
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
ggagccgccc cccggcagaac caccacctt gatctcgagc ttgggtccc 48

<210> 7
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
ggcgccggcg gctccgggtgg tggtggttct caggtaactgc agagtcgg 48

```

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
aatccggagg agacggtgac cgtggtcctt tggccccag 39

<210> 9
<211> 1611
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (11)..(1603)
<223>

<400> 9
gaattccacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca 49
      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr
      1           5               10

gct aca ggt gtc cac tcc gac tac aaa gat gat gac gat aag gat atc 97
Ala Thr Gly Val His Ser Asp Tyr Lys Asp Asp Asp Lys Asp Ile
      15          20            25

cag ctg acc cag tct cca gct tct ttg gct gtg tct cta ggg cag agg 145
Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
      30          35            40            45

gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt gat 193
Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp
      50          55            60

agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa ctc 241
Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu
      65          70            75

ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg ttt 289
Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe
      80          85            90

agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct gtg 337
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val
      95          100           105

gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag gat 385
Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp
     110         115           120           125

```

ccg tgg acg ttc ggt gga ggg acc aag ctc gag atc aaa ggt ggt Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly	130	135	140	433
ggt tct ggc ggc ggc tcc ggt ggt ggt tct cag gtg cag ctg Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser Gln Val Gln Leu	145	150	155	481
cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag att Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile	160	165	170	529
tcc tgc aag gct tct ggc tat gca ttc agt agc tac tgg atg aac tgg Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp	175	180	185	577
gtg aag cag agg cct gga cag ggt ctt gag tgg att gga cag att tgg Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp	190	195	200	625
205				
cct gga gat ggt gat act aac tac aat gga aag ttc aag ggt aaa gcc Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala	210	215	220	673
act ctg act gca gac gaa tcc tcc agc aca gcc tac atg caa ctc agc Thr Leu Thr Ala Asp Glu Ser Ser Thr Ala Tyr Met Gln Leu Ser	225	230	235	721
235				
agc cta gca tct gag gac tct gcg gtc tat ttc tgt gca aga cgg gag Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu	240	245	250	769
250				
act acg acg gta ggc cgt tat tac tat gct atg gac tac tgg ggc caa Thr Thr Val Gly Arg Tyr Tyr Ala Met Asp Tyr Trp Gly Gln	255	260	265	817
265				
ggg acc acg gtc acc gtc tcc tcc gga ggt ggt gga tcc gat atc aaa Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Asp Ile Lys	270	275	280	865
280				
285				
ctg cag cag tca ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys	290	295	300	913
300				
atg tcc tgc aag act tct ggc tac acc ttt act agg tac acg atg cac Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His	305	310	315	961
315				
tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile	320	325	330	1009
330				
aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys	335	340	345	1057
345				

gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu	350	355	360	365	1105
agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr	370	375		380	1153
tat gat gat cat tac tgc ctt gac tac tgg ggc caa ggc acc act ctc Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu	385	390		395	1201
aca gtc tcc tca gtc gaa ggt gga agt gga ggt tct ggt gga agt gga Thr Val Ser Ser Val Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly	400	405	410		1249
ggt tca ggt gga gtc gac gac att cag ctg acc cag tct cca gca atc Gly Ser Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile	415	420	425		1297
atg tct gca tct cca ggg gag aag gtc acc atg acc tgc aga gcc agt Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser	430	435	440	445	1345
tca agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser	450	455	460		1393
ccc aaa aga tgg att tat gac aca tcc aaa gtg gct tct gga gtc cct Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro	465	470	475		1441
tat cgc ttc agt ggc agt ggg tct ggg acc tca tac tct ctc aca atc Tyr Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile	480	485	490		1489
agc agc atg gag gct gaa gat gct gcc act tat tac tgc caa cag tgg Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp	495	500	505		1537
agt agt aac ccg ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys	510	515	520	525	1585
cat cat cac cat cat cat tagtcgac His His His His His His		530			1611

<210> 10
<211> 531
<212> PRT
<213> Homo sapiens

<400> 10

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Tyr Lys Asp Asp Asp Lys Asp Ile Gln Leu Thr
20 25 30

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
35 40 45

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu
50 55 60

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
65 70 75 80

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser
85 90 95

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val
100 105 110

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr
115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Ser Gln Val Gln Leu Gln Gln Ser
145 150 155 160

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys
165 170 175

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln
180 185 190

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp
195 200 205

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr
210 215 220

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala
225 230 235 240

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr
245 250 255

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
260 265 270

Val Thr Val Ser Ser Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln
275 280 285

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys
290 295 300

Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys
305 310 315 320

Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
325 330 335

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu
340 345 350

Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
355 360 365

Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
370 375 380

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
385 390 395 400

Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
405 410 415

Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
420 425 430

Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
435 440 445

Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg
450 455 460

Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe
465 470 475 480

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met
485 490 495

Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn
500 505 510

Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys His His His
515 520 525

His His His
530

<210> 11
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide Linker

<400> 11

Gly Gly Gly Gly Ser
1 5

<210> 12
<211> 4
<212> PRT
<213> Homo sapiens

<400> 12

Asp Tyr Lys Asp
1

<210> 13
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide Linker

<400> 13

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15